

SEQUENCE LISTING

<110> Pang, K.
Lu, K.

<120> METHODS AND REAGENTS FOR TREATING GLUCOSE METABOLIC DISORDERS

<130> CIBT-P02-058

<140> 09/634,363

<141> 2000-08-09

<150> 09/499,526

<151> 2000-02-10

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 108

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(108)

<223>

<400> 1

tac ccc atc aaa ccc gag gct ccc ggc gaa gac gcc tcg ccg gag gag 48
Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

ctg aac cgc tac tac gcc tcc ctg cgc cac tac ctc aac ctg gtc acc 96
Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

B4
cgg cag cgg tac 108
Arg Gln Arg Tyr
35

<210> 2

<211> 36

<212> PRT

<213> Homo sapiens

<400> 2

Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

56

<210> 3
 <211> 1650
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (58)..(1380)
 <223>

<400> 3
 gggcagaggg cacgggcagg cggacgtcgg ggcgccctcg gggaacgtgc gggcacc 57

atg cgt ccc cac ctg tcg ccg ccg ctg cag cag cta cta ctg ccg gtg 105
 Met Arg Pro His Leu Ser Pro Pro Leu Gln Leu Leu Leu Pro Val
 1 5 10 15

ctg ctc gcc tgc gcc gcg cac tcg act gga gcc ctt ccc cga cta tgt 153
 Leu Leu Ala Cys Ala Ala His Ser Thr Gly Ala Leu Pro Arg Leu Cys
 20 25 30

gac gtg cta caa gtg ctg tgg gaa gag caa gac cag tgc ctg cag gaa 201
 Asp Val Leu Gln Val Leu Trp Glu Glu Gln Asp Gln Cys Leu Gln Glu
 35 40 45

ctc tcc aga gag cag aca gga gac ctg ggc acg gag cag cca gtg cca 249
 Leu Ser Arg Glu Gln Thr Gly Asp Leu Gly Thr Glu Gln Pro Val Pro
 50 55 60

ggc tgt gag ggg atg tgg gac aac ata agc tgc tgg ccc tct tct gtg 297
 Gly Cys Glu Gly Met Trp Asp Asn Ile Ser Cys Trp Pro Ser Ser Val
 65 70 75 80

ccg ggc cgg atg gtg gag gtg gaa tgc ccg aga ttc ctc cgg atg ctc 345
 Pro Gly Arg Met Val Glu Val Glu Cys Pro Arg Phe Leu Arg Met Leu
 85 90 95

acc agc aga aat ggt tcc ttg ttc cga aac tgc aca cag gat ggc tgg 393
 Thr Ser Arg Asn Gly Ser Leu Phe Arg Asn Cys Thr Gln Asp Gly Trp
 100 105 110

tca gaa acc ttc ccc agg cct aat ctg gcc tgt gcg gtt aat gtg aac 441
 Ser Glu Thr Phe Pro Arg Pro Asn Leu Ala Cys Ala Val Asn Val Asn
 115 120 125

gac tct tcc aac gag aag cgg cac tcc tac ctg ctg aag ctg aaa gtc 489
 Asp Ser Ser Asn Glu Lys Arg His Ser Tyr Leu Leu Lys Leu Lys Val
 130 135 140

atg tac acc gtg ggc tac agc tcc tcc ctg gtc atg ctc ctg gtc gcc 537
 Met Tyr Thr Val Gly Tyr Ser Ser Ser Leu Val Met Leu Leu Val Ala
 145 150 155 160

ctt ggc atc ctc tgt gct ttc cgg agg ctc cac tgc act cgc aac tac 585
 Leu Gly Ile Leu Cys Ala Phe Arg Arg Leu His Cys Thr Arg Asn Tyr
 165 170 175

atc cac atg cac ctg ttc gtg tcc ttc atc ctt cgt gcc ctg tcc aac 633
 Ile His Met His Leu Phe Val Ser Phe Ile Leu Arg Ala Leu Ser Asn
 180 185 190

57

ttc atc aag gac gcc gtg ctc ttc tcc tca gat gat gtc acc tac tgc	681
Phe Ile Lys Asp Ala Val Leu Phe Ser Ser Asp Asp Val Thr Tyr Cys	
195 200 205	
gat gcc cac agg gcg ggc tgc aag ctg gtc atg gtg ctg ttc cag tac	729
Asp Ala His Arg Ala Gly Cys Lys Leu Val Met Val Leu Phe Gln Tyr	
210 215 220	
tgc atc atg gcc aac tac tcc tgg ctg ctg gtg gaa ggc ctc tac ctt	777
Cys Ile Met Ala Asn Tyr Ser Trp Leu Leu Val Glu Gly Leu Tyr Leu	
225 230 235 240	
cac aca ctc ctc gcc atc tcc ttc ttc tct gaa aga aag tac ctc cag	825
His Thr Leu Leu Ala Ile Ser Phe Phe Ser Glu Arg Lys Tyr Leu Gln	
245 250 255	
gga ttt gtg gca ttc gga tgg ggt tct cca gcc att ttt gtt gct ttg	873
Gly Phe Val Ala Phe Gly Trp Gly Ser Pro Ala Ile Phe Val Ala Leu	
260 265 270	
tgg gct att gcc aga cac ttt ctg gaa gat gtt ggg tgc tgg gac atc	921
Trp Ala Ile Ala Arg His Phe Leu Glu Asp Val Gly Cys Trp Asp Ile	
275 280 285	
aat gcc aac gca tcc atc tgg tgg atc att cgt ggt cct gtg atc ctc	969
Asn Ala Asn Ala Ser Ile Trp Trp Ile Ile Arg Gly Pro Val Ile Leu	
290 295 300	
tcc atc ctg att aat ttc atc ctt ttc ata aac att cta aga atc ctg	1017
Ser Ile Leu Ile Asn Phe Ile Leu Phe Ile Asn Ile Leu Arg Ile Leu	
305 310 315 320	
atg aga aaa ctt aga acc caa gaa aca aga gga aat gaa gtc agc cat	1065
Met Arg Lys Leu Arg Thr Gln Glu Thr Arg Gly Asn Glu Val Ser His	
325 330 335	
tat aag cgc ctg gcc agg tcc act ctc ctg ctg atc ccc ctc ttt ggc	1113
Tyr Lys Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly	
340 345 350	
atc cac tac atc gtc ttc gcc ttc tcc cca gag gac gct atg gag atc	1161
Ile His Tyr Ile Val Phe Ala Phe Ser Pro Glu Asp Ala Met Glu Ile	
355 360 365	
cag ctg ttt ttt gaa cta gcc ctt gcg tca ttc cag gga ctg gtg gtg	1209
Gln Leu Phe Phe Glu Leu Ala Leu Ala Ser Phe Gln Gly Leu Val Val	
370 375 380	
gcc gtc ctc tac tgc ttc ctc aac ggg gag gtg cag ctg gag gtt cag	1257
Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Leu Glu Val Gln	
385 390 395 400	
aag aag tgg cag caa tgg cac ctc cgt gag ttc cca ctg cac ccc gtg	1305
Lys Lys Trp Gln Gln Trp His Leu Arg Glu Phe Pro Leu His Pro Val	
405 410 415	
gcc tcc ttc agc aac agc acc aag gcc agc cac ttg gag cag agc cag	1353
Ala Ser Phe Ser Asn Ser Thr Lys Ala Ser His Leu Glu Gln Ser Gln	
420 425 430	

58

ggc acc tgc agg acc agc atc atc tga gagggctggag cagggtcacc 1400
 Gly Thr Cys Arg Thr Ser Ile Ile
 435 440

catggacaga gaccaagaga ggtcctgcga aggctgggca ctgctgtggg acagccagtc 1460

ttcccagcag acaccctgtg tcctccttca gctgaagatg cccctcccca ggcccttgac 1520

tcttccgaag gatgtgaggc actgtggggc aggacaaggg cctgggattt gggtcgtttg 1580

ctcttctggg aagagaagtt caggggtccc agaaagggac agggaaataa atggttgcct 1640

tgggatgaga 1650

<210> 4

<211> 440

<212> PRT

<213> Homo sapiens

<400> 4

Met Arg Pro His Leu Ser Pro Pro Leu Gln Gln Leu Leu Leu Pro Val
 1 5 10 15

Leu Leu Ala Cys Ala Ala His Ser Thr Gly Ala Leu Pro Arg Leu Cys
 20 25 30

Asp Val Leu Gln Val Leu Trp Glu Glu Gln Asp Gln Cys Leu Gln Glu
 35 40 45

Leu Ser Arg Glu Gln Thr Gly Asp Leu Gly Thr Glu Gln Pro Val Pro
 50 55 60

Gly Cys Glu Gly Met Trp Asp Asn Ile Ser Cys Trp Pro Ser Ser Val
 65 70 75 80

Pro Gly Arg Met Val Glu Val Glu Cys Pro Arg Phe Leu Arg Met Leu
 85 90 95

Thr Ser Arg Asn Gly Ser Leu Phe Arg Asn Cys Thr Gln Asp Gly Trp
 100 105 110

Ser Glu Thr Phe Pro Arg Pro Asn Leu Ala Cys Ala Val Asn Val Asn
 115 120 125

Asp Ser Ser Asn Glu Lys Arg His Ser Tyr Leu Leu Lys Leu Lys Val
 130 135 140

Met Tyr Thr Val Gly Tyr Ser Ser Ser Leu Val Met Leu Leu Val Ala
 145 150 155 160

59

Leu Gly Ile Leu Cys Ala Phe Arg Arg Leu His Cys Thr Arg Asn Tyr
 165 170 175

Ile His Met His Leu Phe Val Ser Phe Ile Leu Arg Ala Leu Ser Asn
 180 185 190

Phe Ile Lys Asp Ala Val Leu Phe Ser Ser Asp Asp Val Thr Tyr Cys
 195 200 205

Asp Ala His Arg Ala Gly Cys Lys Leu Val Met Val Leu Phe Gln Tyr
 210 215 220

Cys Ile Met Ala Asn Tyr Ser Trp Leu Leu Val Glu Gly Leu Tyr Leu
 225 230 235 240

His Thr Leu Leu Ala Ile Ser Phe Phe Ser Glu Arg Lys Tyr Leu Gln
 245 250 255

Gly Phe Val Ala Phe Gly Trp Gly Ser Pro Ala Ile Phe Val Ala Leu
 260 265 270

Trp Ala Ile Ala Arg His Phe Leu Glu Asp Val Gly Cys Trp Asp Ile
 275 280 285

Asn Ala Asn Ala Ser Ile Trp Trp Ile Ile Arg Gly Pro Val Ile Leu
 290 295 300

Ser Ile Leu Ile Asn Phe Ile Leu Phe Ile Asn Ile Leu Arg Ile Leu
 305 310 315 320

Met Arg Lys Leu Arg Thr Gln Glu Thr Arg Gly Asn Glu Val Ser His
 325 330 335

Tyr Lys Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly
 340 345 350

Ile His Tyr Ile Val Phe Ala Phe Ser Pro Glu Asp Ala Met Glu Ile
 355 360 365

Gln Leu Phe Phe Glu Leu Ala Leu Ala Ser Phe Gln Gly Leu Val Val
 370 375 380

Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Leu Glu Val Gln
 385 390 395 400

60

Lys Lys Trp Gln Gln Trp His Leu Arg Glu Phe Pro Leu His Pro Val
405 410 415

Ala Ser Phe Ser Asn Ser Thr Lys Ala Ser His Leu Glu Gln Ser Gln
420 425 430

Gly Thr Cys Arg Thr Ser Ile Ile
435 440
